

FIGURE 1

CGGACGCGTGGGACCCATACTTGCTGGTCTGATCCATGCACAAGGCGGGGCTGCTAGGCCTC
TGTGCCCGGGCTTGGAATTCGGTGCGGATGGCCAGCTCCGGGATGACCCGCCGGGACCCGCT
CGCAAATAAGGTGGCCCTGGTAACGGCTCCACCGACGGGATCGGCTTCGCCATCGCCCGGC
GTTTGGCCCAGGACGGGGCCCATGTGGTCGTCAGCAGCCGGAAGCAGCAGAATGTGGACCAG
GCGGTGGCCACGCTGCAGGGGGAGGGGCTGAGCGTGACGGGCACCGTGTGCCATGTGGGGAA
GGCGGAGGACCGGGAGCGGCTGGTGGCCACGGCTGTGAAGCTTCATGGAGGTATCGATATCC
TAGTCTCCAATGCTGCTGTCAACCCTTTCTTTGGAAGCATAATGGATGTCACTGAGGAGGTG
TGGGACAAGACTCTGGACATTAATGTGAAGGCCCCAGCCCTGATGACAAAGGCAGTGGTGCC
AGAAATGGAGAAAACGAGGAGGCGGCTCAGTGGTGATCGTGTCTTCCATAGCAGCCTTCAGTC
CATCTCCTGGCTTCAGTCCTTACAATGTCAGTAAACAGCCTTGCTGGGCCTGACCAAGACC
CTGGCCATAGAGCTGGCCCCAAGGAACATTAGGGTGAACCTGCCTAGCACCTGGACTTATCAA
GACTAGCTTCAGCAGGATGCTCTGGATGGACAAGGAAAAAGAGGAAAGCATGAAAGAAACCC
TGCGGATAAGAAGGTTAGGCCAGCCAGAGGATTGTGCTGGCATCGTGTCTTTCTGTGCTCT
GAAGATGCCAGCTACATCACTGGGGAAACAGTGGTGGTGGGTGGAGAACCCCGTCCCGCCT
CTGAGGACCGGGAGACAGCCACAGGCCAGAGTTGGGCTCTAGCTCCTGGTGTCTGTTCTCTGC
ATTCACCCACTGGCCTTTCCACCTCTGCTCACCTTACTGTTACCTCATCAAAATCAGTTCT
GCCCTGTGAAAAGATCCAGCCTTCCCTGCCGTCAAGGTGGCGTCTTACTCGGGATTCTCTGCT
GTTGTTGTGGCCTTGGGTAAAGGCCCTCCCCTGAGAACACAGGACAGGCCTGCTGACAAGGCT
GAGTCTACCTTGGCAAAGACCAAGATATTTTTCTGGGCCACTGGTGAATCTGAGGGGTGA
TGGGAGAGAAGGAACCTGGAGTGGAAGGAGCAGAGTTGCAAATTAACAGCTTGCAAATGAGG
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FIGURE 2

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35672
><subunit 1 of 1, 278 aa, 1 stop
><MW: 29537, pI: 8.97, NX(S/T): 1
MHKAGLLGLCARAWNSVRMASSGMTRRDPLANKVALVTASTDGIGFAIARRLAQDGAHVVS
SRKQQNVDQAVATLQGEGLSVTGTVCVHGKAEDRERLVATAVKLHGGIDILVSNAAVNPFFG
SIMDVTEEVWDKTLTDINVKAPALMTKAVVPEMEKRGGSVVIVSSIAAFSPSPGFSPYNVSK
TALLGLTKTLAIELAPRNIRVNCLAPGLIKTSFSRMLWMDKEKEESMKETLRIRRLGEPEDC
AGIVSFLCEDASYITGETVVVGGGTPSRL
```

Important features of the protein:

Signal peptide:

amino acids 1-15

N-glycosylation site.

amino acids 183-186

N-myristoylation sites.

amino acids 43-48, 80-85, 191-196, 213-218, 272-277

Microbodies C-terminal targeting signal.

amino acids 276-278

[illegible]

CGCCCTTGAGCTCCGCCGCCGGGCCGATAGCGCATCGAGAGCGCCTCCGTGAGGACCGAGCGCGGCGCGGGGGCGGCGGGCGAAAGGAGGATGAGGGGGCGCAGCAGCTGCTGACCTGCAGAAACAGGTGGCGCGGCTGGAGGAGGAGAACCGAGACTTTCTGCTGCGCTTGAGGAGCGCCATCGGACGAGTACCAAACTGCGAGCGACGCGCTGCTGAGCAGGAGGAGATGTTGGAACCTGCGGCTGCGGTTAGAGCTGTGTCGGCGCCAGGCTGGGGGGCGCTCGCGGCTCTGAAATGGCTCTCCCTCGGCTCTCTTTGTGCTCGACCTCATACAGCCCCCTGGGGGTGCCACGCCCATGTGCTGGGCATGGTGCGGCTGCTGCTGCTCCTCGGAGATGAAGTTGCTCTGAGCAGAGGGGAGACAGGTGCACAAATGCGAGGAGGCTGGAAGCTGAGTTGCTGACTGAGGTGAACAGGCTGGGAAGTGGCTCTTCAGCTGCTCTCAGAGGAGAGGAGGAGGAGGAGCGCCAGCGCGACCTTACACTGCTGCGCAGAAATAGAGTCAAGCAATGCAGTCAAGAGGCGGGGGCGACGCCAGGGATCTGCGCAGAGAGGAAGGGCCAGAGCTTTGCTTGAGGAAGTTGGATGAGCACTTCCAGGGTCCGAGACGTTTGGTGAGGCAAGGCGAGTTCAGGCTTCAGGCCCGCCAGCTTCCCTCGCCACGCTCAAGTGCGGCTGGCCAGCCAGCAGAGAAGATTCGGGAGCTGATCAACATCCGCATGAAGGAGGAGCTTATGTCGAGCTGTTCCGACAGGAAGGACCTCAGGAGCTGAGCAATGAGCAGCAAGGAGCTTCAGGAGCTGAGCGGCGAGCTGAGTGAAGGCCACAGGCGAGCTGCGGAGACTCGAGGGGCAAGGAGCTCCAGGATGCTGGCGAGCGGTCTCGGCTCCAGGAGTTCCGACAGGAGGTGCTGCGCGCCAGAGCCAGGTGCAAGTGTGAGGAGAGAGGACATCGGAGCGAGCTGATCGAGGAGCTGCTGCTGCGCCAGAGCTGAGAAGCGAGCTGAGTGAAGGACAGGAGCTGAGTGAAGTGAAGCGGAAAGATCGCGGCTCTCCAGAGGAAGGCGAGCTGGAGCGAGCTGGACACGCTGTTGTTGAGCTTGGAAACGCTGCTGAGTCCGCTGAGCCAGCAGGAGCAGGACGCTGCGAGAGGACGGGCTTCGCGAGGAGACGGAGCAGAGAAGCGGCGCTTGAGGGCAGAAATGAGCAAGCGCGAGCACCGCTCAGGAGCTGGAGCTGAGCATGAGCAGAACAGAGAAGCTCTGAAGATTAAGACGGAAAGATCGCGGCTCTCCAGAGGAAGGCGAGCTGGAGCGAGCTGGCAGCAGGCTGTTGTTGAGCTTGGAAACGCTGCTGAGTCCGCTGAGCCAGGAGCAGGACGACGAGAAGATTGAGGAGCAGAAGAAGTGGCTGGACCAGGAGATGGAGAAGTGCTACAGCAGCGCGGGCGCTTGAGGAGCTGGGGGAGAGCTCCAAAGCGGGAGCGGCATCTGGCCAAAGAGGAGCCCTGATGAGCAGAGAAGCAGGGCTGGAGAGCAAGCGCTGAGATCAGCAGCGCCCTCAGCAGGACATCTGCTGCGAGTGTCCAGCGCGCTGGAGCACTTGAGAAGAGCTGTCCGAGAAGACGCGGAGGAGCTGCGGCAGGGCAAGCGCCAGAGCAGCAGCAGATCCGCGGGGAGATCGACAGCGCTGCGCCAGGAGAAGGACTCGCTGCTCAAGCAGCGCTGGAAGTCAAGCGCAAGCTGAGCAGGGAGTGTGTTGCCCGCAGGAGGAGCGGACGCTGTTCCAGTTGATGAGGCAATCAGGCGCTGGATGCTGCACTGAGTATAGATTAAGATGAGGCCATCATATGCCCGCAGCGGGTGCTTCGGCGCTCAGCCTGCTGTCTCCAGTGCAGATGAACCTATGATGCCAAGCTCAGTACCTCTCATCTGACAGACAGAGCGCTCTCTGCAAGTATTTTGACAAGTGGTGACGCTCCGAGAGGAGCAGACACAGCAGCAGATTGCTCTTCGGAAGCTGAGATGCAAGTGAAGGAGCAGAGAGGCTGGTGACTGCTGGAGCTGGCGCTGGAGCGGCGCAGCGCTCGGAGATGAGCCGCAAGCTGACCTGACCTGACAGCAGAGGAGACACGATCAGCATGCTGCTGCGAGCAGCTGCTGCGCAGCAGCTGCGAGCAGCTGCTGTTGAGGAGCAGGGGTCCCCGAGGAACTGAGGCAGCGGGAGGCGGCTGAGCCCCCTGTGGGGCGGGTGCTCTGCTGTGGGTGAGGCAGCGCTGCTGCTGGAATCTTGGCGCTTTGCTCAAGCCCGCGCGGAACTGCAGCAGGCCAGCCCGCGGGATGATGTGATGTCGCGAAAAACCCCTCTAAAGCCTCTGGGGCAGACCTGCTGCTGGAGGAGACTCCGAGCTGCTGAAAGGGGCAAGCTGCTTTTGCTTTGTGAAGGGCAGTCTTACCGCACACCCTAAATCCAGGCCCTCATCTGATCCCTCAGTGGATCAACAAATTTGGGCACTGGCCCAAAGAGATCGGACCCCTATTAAACAAAATAATATGACAAATCCACCACCTACTTCTATGAAGCTGTGGTACCAATTTGCCGCTTGTGCTCTGCTCGAATCTCAGGACAAATCTGTTTTCAGGCGTAAATGGATGTGCTTGTAGTTTCAAGGGTTTGCGCAAGATATCATCAGAAAGGGTCGGTGGCAACAGGTGTGTGTTTAAATGGTCTATGATATATAGGGGAAACTGGGAGACTTTAGGATCTTAAATAAACCAATTTAAATAAAAAAATCTTTGAAGGGG

FIGURE 4

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA47465

<subunit 1 of 1, 830 aa, 1 stop

<MW: 95029, pI: 8.26, NX(S/T): 2

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HLRRNRISNCSQRAGARPGSLPERKGPCLLEELDAAIPGSRAVGGSKARVQARQVPPATAS
EWRLAQAQQKIRELAINIRMKEELIGELVRTGKAAQALNRQHSQRIRELEQEAEQVRAELSE
GQRQLRELEGKELQDAGERSRLQEFRRRVAAAQSQVQVLKEKKQATERLVLSAQSEKRIQE
LERNVQLMRQQGQLQRRRLREETEQQKRRLEAEMSKRQHRVKELELKHEQQQKILKIKTEEIA
AFQKRKRRSGNSGVSLEQQQKIEEQKKWLDQEMEKVLQORRALEELGEELHKREAILAKKE
ALMQEKTGLESKRLRSSQALNEDIVRVSSRLEHLEKELSEKSGQLRQSGSAQSQQQIRGEIDS
LRQEKDSLKQRLIDGKLRQGSLLSPEEERTLFQLDEAIEALDAAIEYKNEAITCRQRVLR
ASASLLSQCEMNLMAKLSYLSSETRALCKYFDKVVTLREEQHQQQIAFSELEMQLEEQQR
LVYWLEVALERQRLEMDRQLTLQQKEHEQNMQLLLQQSRDHLGEGGLADSRQYEARIQALEK
ELGRYMWINQELKQKLGGVNAVGHSGGEEKRSLCSEGRQAPGNEDELHLAPPELLWLSPLTEG
APRTREETRDLVHAPLPLTWKRSSLCGEEQGSPEELRQREAAEPLVGRVLPVGEAGLPWNFG
PLSKPRRELRRASPGMIDVRKNPL

Important features:

Leucine zipper pattern.

amino acids 557-579, 794-815

N-glycosylation sites.

amino acids 133-136, 383-386

Kinesin related protein Kif-4 Coiled-coil domain:

amino acids 231-672

FIGURE 5

ATTCTCCTAGAGCATCTTTGGAAGCATGAGGCCACGATGCTGCATCTTGGCTCTTGTCTGCT
GGATAACAGTCTTCCTCCTCCAGTGTTCAAAAGGAACACAGACGCTCCTGTTGGCTCAGGA
CTGTGGCTGTGCCAGCCGACACCAGGTGTGGGAACAAGATCTACAACCCTTCAGAGCAGTG
CTGTTATGATGATGCCATCTTATCCTTAAAGGAGACCCGCCGCTGTGGCTCCACCTGCACCT
TCTGGCCCTGCTTTGAGCTCTGCTGTCCCGAGTCTTTTGGCCCCCAGCAGAAGTTTCTTGTG
AAGTTGAGGGTTCTGGGTATGAAGTCTCAGTGTCACATTATCTCCCATCTCCCGAGCTGTAC
CAGGAACAGGAGGCACGTCTGTACCCATTAAAAACCCAGGCTCCACTGGCAGACGGCAGAC
AAGGGGAGAAGAGACGAAGCAGCTGGACATCGGAGACTACAGTTGAACTTCGGAGAGAAGCA
ACTTGACTTCAGAGGGATGGCTCAATGACATAGCTTTGGAGAGGAGCCCAGCTGGGGATGGC
CAGACTTCAGGGGAAGAATGCCCTTCCTGCTTCATCCCCTTCCAGCTCCCCTTCCCGCTGAG
AGCCACTTTCATCGGCAATAAAATCCCCCACATTACCATCT

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA57700
><subunit 1 of 1, 125 aa, 1 stop
><MW: 14198, pI: 9.01, NX(S/T): 1
MRPRCCILALVCWITVFLQCSKGTDDAPVGSGLWLCQPTPRCGNKIYNPSEQCCYDDAILS
LKETRRCGSTCTFWPCFELCCPESFGPQQKFLVKLRVLGMKSQCHLSPISRSCTRNRRHVLYP
```

Important features:

Signal sequence

amino acids 1-21

N-myristoylation sites.

amino acids 33-39, 70-76

FIGURE 7

CCCACGCGTCCGCCCCACGCGTCCGGGTGCCACTCGCGCGCCGGCCGCGCTCCGGGCTTCTCT
 TTTCCCTCCGACGCGCCACGGCTGCCCAGACATTCCGGCTGCCGGGTCTGGAGAGCTCCCCG
 AACCCCTCCGCGGAGAGGAGCGAGGCGGCGCCAGGGTGGCCCCCGGGGCGCGCTTGGTCTCG
 GAGAAGCGGGGACGAGGCCGAGGATGAGCGACTGAGGGCGACGCGGGCACTGACGCGAGTT
 GGGGCCGCGACTACCGGCAGCTGACAGCGCGATGAGCGACTCCCAGAGACGCCCTAGCCCCG
 GTGTGCGCGCCAGGCGGAGCGCGCAGGTGGGGCTGGGCTGTTAGTGGTCCGCCCCACGCGGG
 TCGCCGCGCGGCCAGGATGGGCGCTGGCAACCCGGGCCCGCGCCCGCGCTGCTACCCCTG
 CGCCCGCTGCGAGCCCGCGCTCCGGCCCGCGCCCTGCGCTCATGGACGGCGGCTCCCGGCTG
 GCGGCGGCGCGCCCCCGGGCTGTGAATGCGACTCGCCCCCTCGGCCGCGCTCCCGCCCGCCC
 GCCCGCCGGGACGTGGTAGGGGATGCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCA
 GTTCCCTCCTGGTCACTTGTGCTGATGGTGGCTCTGTGCAGTCCGAGCATCCCGCTGGAG
 AAGCTGGCCCCAGGCACCAGAGCAGCCGGGCCAGGAGAAGCGTGAGCACGCCACTCGGGACGG
 CCCGGGGCGGGTGAACGAGCTCGGGCGCCCGCGAGGGACGAGGGCGGCAGCGGCCGGGACT
 GGAAGAGCAAGAGCGGCCGTGGGCTCGCCGGCCGTGAGCCGTGGAGCAAGCTGAAGCAGGCC
 TGGGTCTCCCAGGGCGGGGGCGCCAAGGCCGGGGATCTGCAAGTCCGGCCCCCGGGGACAC
 CCCGAGGCGGAAGCCCTGGCCGAGCCGCCAGGACGCGATTGGCCGGAACTCGCGCCCA
 CGCCCGAGCCACCCGAGGAGTACGTGTACCCGGACTACCGTGGCAAGGGCTGCGTGGACGAG
 AGCGGCTTCGTGTACGCGATCGGGGAGAAGTTCGCGCCGGGCCCTCGGCCCTGCCCGTGCT
 GTGCACCGAGGAGGGGCGCGTGTGCGCGCAGCCGAGTGCCCGAGGCTGCACCCGCGCTGCA
 TCCACGTGACACGAGCCAGTGTGCCCGCAGTGCAAGGAGAGGAAGAACTACTGCGAGTTC
 CGGGGCAAGACCTATCAGACTTTGGAGGAGTTCGTGGTGTCTCCATGCGAGAGGTGTCGCTG
 TGAAGCCAACGGTGAGGTGCTATGCACAGTGTGAGCGTGTCCCAGACGGAGTGTGTGGACC
 CTGTGTACGAGCCTGATCAGTGTCTCCATCTGCAAAAATGGTCCAACTGCTTTTGAGAA
 ACCGCGGTGATCCCTGCTGCGAGAGAAGTGAAGACTGACGAGTGACCATATGCCACTGTAC
 TTATGAGGAAGGCACATGGAGAATCGAGCGCAGGCCATGTGCACGAGACATGAATGCAGGC
 AAATGTAGACGCTTCCAGAAACAAAACTGTGACTTTTTCTAGAACATTTTACTGATGTGAA
 CATTCTAGATGACTCTGGGAACTATCAGTCAAAGAAGACTTTTGATGAGGAATAATGAAAA
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FIGURE 8

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AAAQDAIGPELAPTEPPEEYVYPDYRGKGCVDSESGFVYAIGKFAFGPSACPLCTEEGPL
CAQPECPRHLPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVS PCERCRC EANGEVL
CTVSACPQTECVDPVYEPDQCCPICKNGPNCFAETA VIPAGREVKTDECTICHCTYEETWR
IERQAMCTRHECRQM
```

Important features of the protein:

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 11-30

Glycosaminoglycan attachment site.

amino acids 80-83

N-myristoylation sites.

amino acids 10-15, 102-107, 103-108

Cell attachment sequence.

amino acids 114-117

EGF-like domain cysteine pattern signature.

amino acids 176-187

FIGURE 9

CAGCCACAGACGGGTCAATGAGCGGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCAC
TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA
CACGTTGATGCTCAATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG
AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC
TCCTACACCTTCGTGTGCCGCCAGGAGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGTCTGCTTGCTATGG
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GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
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GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCTGGTGGGGACAAAAG
GCTGCAGCACTGTTGGGGCTCAAATTTCCAGAAGACCACCATCCACTCAGCCCCCTCTGGG
GTGCTTGTCGCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
CAGCGTTCTGCTGAACCTCCTCCCTCCTCAAGCTGCCCCCTGTCCAGGAGACCGGCAGTGTC
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CCATTCTGTCCATGAATCATCTTCCCCACACAAATCATTATCTACTCACCTAACAGCA
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FIGURE 10

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PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRRLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGTGKCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN
SLPPQAAVPVPGDRQCPTCVQPLGTCCSSGSPRMTCPRGATHCYDGYIHLGGGLSTKMSIQGC
VAQPSSFLNLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLES�TWGVGLALAPALWWGVVCPSC
```

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 243-260

N-glycosylation sites.

amino acids 46-49, 189-192, 382-385

Glycosaminoglycan attachment sites.

amino acids 51-54, 359-362

N-myristoylation sites.

amino acids 54-59, 75-80, 141-146, 154-159, 168-173, 169-174,
198-203, 254-259, 261-266, 269-274, 284-289, 333-338, 347-352,
360-365, 361-366, 388-393, 408-413, 419-424

FIGURE 11

CGACGATGCTACGCGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCTGCGCGCGGCCCTG
GCTGCGCGGCTGCTCTCGTTCGCTTGCGCGCTGCTCTCTTCTAGAGCCGAGGGGACCCGGTGGC
CTCGTTCGCTCAGCCCCCTATTTCGGCACCAAGACTCGCTACGAGGATGTCAACCCCGTGCTAT
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CAGCTGGTGCCTCATTTGCGCCACGGCACCCGCTACCCACGGTCAACAGATCCGCAAGCT
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GCAGCCGCGACCTGGGTGCAGCGCTGGCCGACTGGCCCTTTGTGGTACGCGGACTGGATGGAC
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CTTCCCGGCCCTTTTCAGCCGTGAGAACTACGGCCGCTGCGGCTCATCACCAGTTCCAAGC
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CACTTGGCTTCGATTTTTATATTTTCTATTATATGAAATGTATCTTTTGGTGTGTTGATTT
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FIGURE 12

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RDLGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHR
CMDSSAAFLQGLWQHYHPLPPPDVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYH
VEAFKTPGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCSFDLAIKGVKSPWCDVFDIDDA
KVLEYLNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAE
TLLPLLSLMGYFKDKEPLTAYNYKKQMRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRV
QMLLNEKVLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSEDEL
```

Important features:

Signal sequence

amino acids 1-30

N-glycosylation sites.

amino acids 242-246, 481-485

N-myristoylation sites.

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

Endoplasmic reticulum targeting sequence.

amino acids 484-489

FIGURE 13

GGGACTACAAGCGCGCGCGCTGCCGCTGGCCCTCAGCAACCCCTGCAGATGGCGCTGAGGCGGCCACCGCGAC
 TCCGGCTCTGCGCTCGCGCTGCCGCTTCTTCTCTGCTGCTGCTTTTCAGGGGCTGCCGTAGTAGGGGCTGTAAATC
 TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTTGAAAGTGTGGAACTGTCTTGCATCATTACGGATTTCG
 AGACAAGTGCACCCAGGATCGAGTGGGAAGAAAATCAAGATGAACAAACACATATGTGTTTTTGACACAGAAA
 TTCAGGGAGACTCTGGCGGTGCTGCAGAAATACTGGGAAGACATCCCTGAAGATCTGGAATCTGCAGACGGAGAG
 ACTCAGCCCTTTATCGCTGTGAGGCTGCTGCTCGAAATGACCGCAGGAAATGTATGATAGTTGTGATCGAGTTAA
 CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTCCGAAGGCTGTACAGTAGGACAGATGGCCACACTGCG
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 CCAGAGCCAAATCCAGATTTTCGCAATTTCTTTTCCACTTAAACTCTGAAACAGGCACCTTTGGTGTCTACTGCTG
 TTTCAAGAGGACGACTCTGGGCGAGTACTGTCATTGGTTTCCAATGACGCGGCTCAGCCAGGTGTGAGGAGCAGG
 AGATGGAAGTCTATGACCTGGAACATTTGGCGGAATTTATTTGGGGGGTTCCTGGTTGCTTGTCTGATCGCCCTGA
 TCACTGTGGGCATCTGCTGTGCATACAGACGTGGCTACTCATCAACAATAAACAGGATGGAGAAGTTACAAGA
 ACCAGGGGAAACAGATGGAGTTAACTACATCCGCATGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTG
 TGATCTGAAGACCCCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAAATCTCTGTCAA
 GGCAGCGAGAGCTGTGTCACCTGGACAGAGTACAGACTCATCAGAACTTTTCGATTTTGGCCAAAGTTGACCA
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 CAGCAGCCACGACAGCACCATTGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGGCGGGAACCCA
 GAAAAGGCTTTCTACACAGCAGCCTTACTTCATCGGCCACAGACACCAACCGCAGTTTCTTCTTGAAGGCTCTGC
 TGATCGGTTTGGACGTGTCATTGTGGAGAACTTTTGGATCAGCATTTTGTAAAAACAACCAAAATCAGGAAG
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 TACATCTAAATTTTGTCTAAGGATGTATTTTGTATTGATTGAAAGAAAATTTCTATTATAACTGTAAATATATTGT
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 TGGAAAATATCAATAATTAAAGATATTTTACCACAGGAATCTCTCATGGAAGTTTACTGTGATGTTCTCTTTCT
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 AAGATTGCTCAAGGCCAAGGCAATTCGCAAAATCAAGTCTGTCAAGTACAATAACATTTTAAAAAGAAAATGGAT
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 GGAATGGCGGCCAGTCCAGCCTTTTAAAGAACGTGAGTGGAGCGCCAGGTGGAAGGCTGCGCGGAGGAGAAAG
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 CGGAAGAAAGAAATACCTGCTGATTTTAAAGATGAATGTGACTCAAGACTTTGAGCCGATGACGAGGCTGTGATTCT
 GCCTTTGGATGGATGTTGTCTGTACACAGATGCTACAGACTGTACTAACACACCGTAATTTGGCATTTGTTTAAAC
 CTCATTTATAAAGCTTCAAAAAACCCA

FIGURE 14

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSCLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDNLNIGGIIIG
VLVVLAVLALITLGICAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
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Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

FIGURE 15

CAGGACCAGGTTCTTCTACGCTGGAGCAGCGGGAGACAGCCACCATGCACATCTCTGTTGGTCCATGCCATGGTG
 ATCTCTGCTGAGCTGGGGCCCGCTCGAGCCGACGACGAGCTTCAGGCGCTGCTGGACATCTGGTTTCCGGAG
 GAGAAGCCATGCCCCACCCGCTTCTCGTGGTGGACATCATCGAGGAGGCGCTGCTGCTTCTGACTGGCTGAAGCTG
 CGCATGATCCGTTCTGAGGTGCTCCGCCCTGGTGAGCGCCGCTCGCAGGACCTGGAGCGCCGAGCAGCTGCTGCTG
 TTCGTGACATCGTTTGGCATCCCGCTGTCCAGCATGAGCAAACTCTCCAGTTCTCGGACGAGCAGTGGCCAC
 GACCCCGACATCTGGAGCAGAAATCATGGACAAGAATTATACATGGCCCACTGTTGGTGAAGGTCCAGCATGAGCGC
 GGCGCTCTCGGAGGCCAGACTTTCCACTCTTGTCTCACAGCCTTCCCTGCGCCGCCCGCGAGACACAGAGGCA
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 GAGGTGCCGGGCATCAGCGTGCCTGCTCGAGGCCCTCGCCACCTCTGCTCAGCTCCCCACACGGCGGTGCCTG
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 GGGCTGATCAGAGTGAGGTGCCCCACCTGGAGGAGTGTCTGATGCTCTTCTGCCACTCGGATGCTGCTG
 TCCCCTTTTCAGCCTGTAAAGCCGTTGTGGTGGTGAAGCTCCCTGCTGCTGAGGAGGAGGAGCCCTGGCTGGG
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 TTCTCTGGGCTGCATCATGTTCTCTCGCATCTGGCAGGGGCGGGACACGCGCACCCCGCAGAAAGCGGCGGAG
 GAGCTGGTGTGCGGGTCCAGGGCCCGGAGCTCATCAGCCTGGTGGAGCTGATCTTGGCCGAGGCGGAGACCGGG
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 GACGATGAGAGTGTACGAAAGTGTACGGAGCACCTGTGAGGTGCATTCAGCAGTGGGGAGACAGCGTGTGGGA
 AGGCGCTGCCGAGACCTTCTCTGCACTCTACCTACAGCGGCCGAGCTGCGGGTGGCCGTGCTGAGGTCTTA
 CTGCACAGCGAAGGGCTGCCAGCAGCAGCGTCTGCAAGCTGGACGGACTCATCCACCGCTTCACTACGCTCTT
 GCGGACACCGAGCTCCCGGGCGTTGGAGAACCGAGGGCGGATGCCAGCATGGCCTCCGGAAGCTGGCGGTG
 GCGCACCGCTGCTGCTGCTCAGGCACCTGCCATGATCGCGGCGCTCTGACAGCGCGCACCCACCTCAACTT
 CAGGAGTTCCGSCAGCAGAACCACCTGAGCTGCTTCTGCACTGCTGGGCTGCTGGAGCTGCTGCAAGCCGAC
 GTGTTCCGAGCAGACACAGGGGGCGCTGTGGAGCTGCTTCTGTCTCTCATCCGCTGCTGCTGAATTACAGG
 AAGTCTCTCCGCCATCTGGCTGCCTTTCATCAACAAGTTTGTGAGTTCATCCATAAGTACATTACCTACAATGCC
 CCAGCAGCATCTCTCTCTGCAAGACACGCCGACCCGCTCCACGACCTGTCTGCAACAGCTGCTGCTGCTGCTG
 ATGCTGAAATCCCTCTTTCAGGGCTCAGCCTGCCAGCAGGAGCAGCAGGACCGACCGAGGCTGGACGAAGAG
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 GAGATGTCCCGGAGACCCAGATCTCTGAGCTTCTCTCGACCAACCTGCAGCGGCTGATGAGCTCGGCCGAG
 GAGTGTTCGCGCAACCTCGCTTTCAGCTGGCCCTGCGCTCCATGCAGAACAGCCCGACATTGGCAGCGCTTTT
 CTGCGCCAGTTTACTGTACTGCTGGGAGCAGCAGGACTTTGAGGTGGTGCAGAGGCCCTTCGGGAACCTGCCTGAG
 TACGCTCTCTGTCAGAGCAGCGGCTGTGCTGCTCACCGGCTCTCTGTTGGGATGTACGCGCAGATG
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 CCCCCTCCAAAGCCCGGCCCTCCCTGCCCGGGATCTCGAGGCAAAAGCCCAAGGAGGTGGGCGTTGCTGG
 TCTGTCCGAGGAGGTGAGGGCGCCGAGCCCTGAGGCCAGGCGCCAGGAGCAATCTCCGAGCACTCGGGGTGG
 CTCGCGGCGCGCGTGGCATAGGGCGCTCCAGCAAGCCCTCATTCACCTTCTGGGCGACAGCCCTGCCGCG
 AGCGGGGATCCCCCGGCATGGCTGGGCTGGTTTGAATGAACGACCTGAACGTGTCAA

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FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77631

><subunit 1 of 1, 1029 aa, 1 stop

><MW: 114213, pI: 6.42, NX(S/T): 0

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IRSEVLRLVDAALQDLEPQQLLLFVQSFGIPVSSMSKLLQPLDQAVAHDPQTLEQNIMDKNY
MAHLVEVQHERGASGGQTFHSLLTASLPPRRDSTEAPKPKSSPEQPIGQGRIRVGTQLRVLG
PEDDLAGMFLQIFPLSPDPRWQSSSPRPVALALQQALGQELARVVQGSPEVPGITVRVLQAL
ATLLSSPHGGALVMSMHRSHFLACPLLRLQCQYQRCVPQDTGFSSFLFKVLLQMLQWLDS PG
VEGGPLRAQLRMLASQASAGRRLSDVRGGLLRLAEALAFRQDLEVVSSTVRAVIATLRSGEQ
CSVEPDLISKVLQGLIEVRSPHLEELLTAFFSATADAASPPACKPVVVVSSLLQEEEP
GGKPGADGGSLEAVRLGPSSGLLVDWLEMLDPEVVSSCPDLQLRLLFSSRRKGGKQAQVPSFR
PYLLTLFTHQSSWPTLHQCIIRVLLGKSREQRFPDSASLDFLWACIHVPRIWQGRDQRTPPQKR
REELVLRVQGPELISLVELILAEAETRSQDGDTAACSLIQARLPLLLSCCGDDESVRKVTE
HLSGCIIQWGD SVLGRRCRDL LLQLYLQRPELRVPVPEVLLHSEGAASSSVCKLDGLIHRFI
TLLADTSDSRALENRGADASMACRKLAVAHPLLLLRHLPMIAALLHGRTHLNFQEFRRQONHL
SCFLHVLGLLELLQPHVFRSEHQGALWDCLLSFIRLLLNRYKSSRLHAAIFNKVQFIHKYI
TYNAPAAISFLQKHADPLHDLSPDNLDLMLKSLLAGLSLPSRDDRTDRGLDEEGEESSAG
SLPLVSVSLFTPLTAAEMAPYMKRLSRGQTVEDLLEVLSDIDEMSSRRRPEILSFFSTNLQRL
MSSAECCRNLAFLASLALRSMQNSPSIAAFLPTFMYCLGSDQFPEVVQATALRNLPEYALLCQE
HAAVLLHRAFLVGMYGQMDPSAQISEALRIILHMEAVM

Important features:

Signal peptide:

amino acids 1-16

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

N-myristoylation sites.

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449,
665-671, 698-704

Amidation sites.

amino acids 329-333, 634-638

[illegible]

CCGGGCCATGCGACCTTCGGCCCCCGGGCGCGCGCCGCGACCCGAGGAGATGAGGCTCCGC
AATGCGCACTTCTGAGCTGCTGCTTCTTCTGCTGTGCGCTTCTCTCGCTGTCTCGGTA
CGCGGCATTCGCGGCCAGAAAGGCGAGCTTGAGACGTTTACAGCGGGAGTCTTCTGGCG
TGC CGCATCGGTTGCACGCACTGAGCAGGAGAGCCTCAAGCGCTCCAAGGAGCTCAACCTG
GTGCTGGACGAGATCAAGAGGGCCGTGTCAAGAAAGGACGGCGTGCAGCGGAGACCGGAA
TCGCACCTGGGGCCGCTTAACAGAGGACCCCCGATTTGAAGCCGTGGAAACGGCTCACACGGG
ACGTGCTGCACCTGCCACCGTCTTCCATCACTGTGCCACACCTGCTGGCCAAGGAGAGCACT
CTGCAACCCGCGGTTGAGCTTGGGCCAAGGCGCGACCGGAGTGTCGGTGTGATGGGCATCCC
GAGCGTGGCGGCGAGGTGCATCTGCTACCTGACACTGACACTGTGCATCTGCTCATCTCCGAGC
TGAGCCCGCAGGAGAAGGAGGACTCGGTCACTCGTGGTGCTGATGCGCGAGACTGACTCACAG
TACACTTCGCGAGTGACAGAGAACATCAAGGCCTTGTTCACCGAGAGATCCATTCTGGGCT
CCTGGAGGTTATCTCACCTCCCCCACTTACCTGACTTCTCCGCTCCGAGAGTCTCT
TTGGGAGCCCAAGGAGAGTCAAGTGGAGGACCAACAGAACCTCGATTGCTTCTCT
ATGATGTACGCGCAGTCCAAAGGCATCTACTACGTGCAGCTGGAGGATGACATCGTGGCCAA
GCCCAACTACTCTGAGCACCATGAAGAACTTTGCACTGCAGCAGCTTCAGAGGACTGGATGA
TCCTGGAGTTCTCCAGCTGGGCTTCAATTGTAAGATTTCAAGTCGTGGACCTGAGCCCTG
ATTGTAGAGTTCACTTCTATGTTCTACCGGCAAGGCCATGCATGGCTCTGCAGCATAT
TCTGTGGGTGAAAGTCTGCAACCCCGAGAAGGATGCGAAGCACTGTGACCCGCGAGAAAGCA
ACCTCGCGGATCCGCTTCAAAACCGTCCCTCTTCGACACGTTGGGCACTGCCTGCTGCTGGCT
GGCAAGATCCAGAACTGAAGGACAAAGACTTTGAAAGCAGGCGCTGCGAAGAGCATGT
GAACCCGCGCAGAGGTTGACACGAGCCTGAAGACATACCAGCACTTACCCTGGAGAAAG
CTACCTGCGCGAGGACTTCTTGGGCTTCAACCTGCGCGGGGAGACTTCATCCGTTCT
CGCTTCTTCAACCTCTAAGACTGAGCGGCTTCTTCTCCGAGTGGGAACATCGACACCC
GGAGGACAAGCTCTTCAACACGTCTGTGGAGGTGCTGCCCTTCGACAACCTCAGTCAGACA
AGGAGGCCCTCGAGGAGGGCGCGACGCCACCTCCGGTACCTCGAGCGCCCGACGGCTAC
CTCAGATCGGCTCTTCTACAAGGAGTGGCAGGAGGAGGTGGACCCAGCTTCGGCCG
TCTGGAAGCACTGCGCCTCTCGATCCAGACGGACTCCCTGTGTGGGTGATTCTGAGCGAGA
TCTTCTGAAAAAGGCGCATTAAGCTGCGGGCTTCTGAGGGTACCTGTGGCGACGCTTGAA
GCCCACTTCTTGGGGGTGTCGCTACTGCGGCTCCCCGGAGGGCGAGATCGGCCCGCCCAA
AGGTTCTTGCCTGCGGTGCGGCTTGGGCGGCTTGGGTCGCGCGCTGGCCCCGAGGCCCTTA
GGAGCTGTTGCTGCCCCCGCCGCGGGCGCGGAGGAGCGCGCGGCCCCACACTGTGCC
TGAGGCCCGGAACCTGTCGACACCGGCTGCCCACTGAGGCGGCTTTAGAAGGCTTTTAT
TTGGGCGGCCCGCTCTTGGCGCGCAACTCGAATGCATATACTACTTTATGTGCTGTTAT
TTTTATTCTTGGATACATTTGATTTTTTACGTAAGTCCACATATACTTCTATAAGAGCGTG
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AAAAAAAAAAAAAAAAAAAA

FIGURE 18

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA82307
><subunit 1 of 1, 548 aa, 1 stop
><MW: 63198, pI: 8.10, NX(S/T): 4
MRLRNGTFLTLLLFCLCAFLSLSWYAALSGQKGDVVDVYQREFLALRDLHAAEQESLKRSK
ELNLVLDEIKRAVSERQALRDGDGNRTWGRLTEDPRLKFWNGSHRHVLHLPTVFHHLPHLLA
KESSLQPAVRVGQGR TGVSVMGIPSVRREVHSYLTDTLHSLISELSPQEKEDSVIVVLIAE
TDSQYTSAVTENIKALFPTEIHSGLLEVISPSPHFYPDFSRLRESFGDPKERVRWR TKQNL D
YCFLLMYAQSKGIYYVQLEDDIVAKPNYLSTMKNFALQQPSEDWMILEFSQLGFIGKMFKSL
DLSLIVEFILMFYRDKPIDWLLDHILWVKVCNPEKDAKHCDRQKANLRIRFKPSL FQHVGTH
SSLAGKIQKLKDKDFGKQALRKEHVNPPAEVSTSLKTYQHFTLEKAYLREDFFWAFTPAAGD
FIRFRFFQPLRLERFFFRSGNIEHPEDKLFNTSVEVLPFDNPQSDKEALQEGR TATLRYPRS
PDGYLQIGSFYKCVAEGEVDPAFGP LEALRLSIQTDSPVWVILSEIFLKKAD
```

Important features:

Signal sequence

amino acids 1-23

N-glycosylation sites.

amino acids 5-9, 87-91, 103-107, 465-469

N-myristoylation sites.

amino acids 6-12, 136-142, 370-376, 509-515